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CAS REGISTRY NUMBERS AND CHEMICAL NAMES (CNs) PRESENT
FROM JANUARY 1969 TO DATE.

RECORDS LAST ADDED: 22 January 2003 (20030122/ED)


=> s Jablonski S A/AU and Journal of Virology/so and 1991/py
             6 JABLONSKI S A/AU
       1854566 JOURNAL/SO
       4672338 OF/SO
         41173 VIROLOGY/SO
         12377 JOURNAL OF VIROLOGY/SO
                 ((JOURNAL(W)OF(W)VIROLOGY)/SO)
        545130 1991/PY
L1           0 JABLONSKI S A/AU AND JOURNAL OF VIROLOGY/SO AND 1991/PY

=> s morrow c d/au and journal of virology/so and 1991/py
            43 MORROW C D/AU
       1854566 JOURNAL/SO
       4672338 OF/SO
         41173 VIROLOGY/SO
         12377 JOURNAL OF VIROLOGY/SO
                 ((JOURNAL(W)OF(W)VIROLOGY)/SO)
        545130 1991/PY
L2           0 MORROW C D/AU AND JOURNAL OF VIROLOGY/SO AND 1991/PY

=> e jablonski s a/au
E1           2     JABLONSKI RYSZARD/AU
E2          11     JABLONSKI S/AU
E3           6 --> JABLONSKI S A/AU
E4           1     JABLONSKI S K/AU
E5           2     JABLONSKI SANDRA/AU
E6          13     JABLONSKI SANDRA A/AU
E7           1     JABLONSKI SHARON/AU
E8           1     JABLONSKI STEFAN/AU
E9           1     JABLONSKI STIEMKE M M/AU
E10          2     JABLONSKI STIEMKE MONICA M/AU
E11          4     JABLONSKI T/AU
E12          1     JABLONSKI TRACEY/AU

=> s E2 and E3
            11 "JABLONSKI S"/AU
             6 "JABLONSKI S A"/AU
L3           0 "JABLONSKI S"/AU AND "JABLONSKI S A"/AU

=> s e3
L4           6 "JABLONSKI S A"/AU

=> s e2
L5          11 "JABLONSKI S"/AU

=> e morrow c d/au
E1           1     MORROW C A/AU
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E3           43 --> MORROW C D/AU
E4           24      MORROW C E/AU
E5            3      MORROW C F/AU
E6            1      MORROW C F JR/AU
E7            1      MORROW C H/AU
E8           62      MORROW C J/AU
E9            1      MORROW C J JR/AU
E10           1      MORROW C K/AU
E11           1      MORROW C L/AU
E12           2      MORROW C M/AU

=> s e3
L6           43 "MORROW C D"/AU

=> s poliovirus
L7         6736 POLIOVIRUS

=> s polio
L8         3331 POLIO

=> s l6 and l7
L9           18 L6 AND L7

=> s l5 and l7
L10           0 L5 AND L7

=> s (rna dependent rna polymerase)
         371623 RNA
         620788 DEPENDENT
         371623 RNA
         185045 POLYMERASE
L11         999 (RNA DEPENDENT RNA POLYMERASE)
                  (RNA(W)DEPENDENT(W)RNA(W)POLYMERASE)

=> s (mutant? or mutation?)
         210873 MUTANT?
         227210 MUTATION?
L12      369996 (MUTANT? OR MUTATION?)

=> s l7 and l11 and l12
L13          23 L7 AND L11 AND L12

=> s attenu?
L14       90538 ATTENU?

=> s l13 and l14
L15           1 L13 AND L14

=> d l15 bib ab

L15  ANSWER 1 OF 1  BIOSIS  COPYRIGHT 2003 BIOLOGICAL ABSTRACTS INC.
AN   1995:436870  BIOSIS
DN   PREV199598451170
TI   Elongation activity of poliovirus RNA polymerase derived from
     Sabin type 1 sequence is not temperature sensitive.
AU   Baker, Susan; Richards, Oliver C.; Ehrenfeld, Ellie (1)
CS   (1) Dep. Molecular Biol. Biochem., Univ. California Irvine, Irvine, CA
     92717 USA
SO   Journal of General Virology, (1995) Vol. 76, No. 8, pp. 2081-2084.
     ISSN: 0022-1317.
DT   Article
LA   English
AB   Determinants of attenuation in the Sabin type 1 strain of
```

poliovirus are located in the 5' noncoding region, the capsid coding region and the viral **RNA-dependent RNA polymerase** (3D-pol) coding region. These **mutations** also contribute to a temperature sensitive phenotype of virus replication. We have cloned and expressed the Sabin 1 virus 3D-pol protein which contains three amino acid differences from the wild-type (Mahoney) sequence, as well as a wild-type polymerase containing only a single Sabin amino acid substitution at nt 6203. These enzymes have been examined and compared for temperature sensitive polymerase activity. Wild-type and mutated polymerases demonstrated identical specific activities at 30, 35 and 39 degree C. All three showed the same kinetics of heat inactivation after pre-incubation at elevated temperatures. Thus the contribution of Sabin 3D-pol sequences to the inability of the virus to grow at elevated temperatures must lie in a function or activity of the enzyme other than RNA polymerization. A likely reaction is the initiation step of RNA chain synthesis.

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=> s rever?
L16     304786 REVER?

=> s l7 and l11 and l16
L17          10 L7 AND L11 AND L16

=> d 1-10 bib ab

L17  ANSWER 1 OF 10  BIOSIS  COPYRIGHT 2003 BIOLOGICAL ABSTRACTS INC.
AN   2003:4334  BIOSIS
DN   PREV200300004334
TI   Modulation of hepatitis C virus RNA-dependent
     RNA polymerase activity by structure-based site-directed
     mutagenesis.
AU   Labonte, Patrick; Axelrod, Vladimir; Agarwal, Atul; Aulabaugh, Ann; Amin,
     Anthony; Mak, Paul (1)
CS   (1) Wyeth Research, 85 Bolton St., R231A, Cambridge, MA, 02140, USA:
     makp@wyeth.com USA
SO   Journal of Biological Chemistry, (October 11 2002) Vol. 277, No. 41, pp.
     38838-38846. print.
     ISSN: 0021-9258.
DT   Article
LA   English
AB   The hepatitis C virus (HCV) encodes an RNA-dependent
     RNA polymerase (NS5B), which is indispensable for the
     viral genome replication. Although structural comparison among HCV NS5B,
     poliovirus 3D-pol, and human immunodeficiency virus-
     reverse transcriptase RNA-dependent polymerase reveals the
     canonical palm, fingers, and thumb domains, the crystal structure of HCV
     NS5B highlights the presence of a unique A1-loop, which extends from the
     fingers to the thumb domain (amino acids 12-46), providing many contact
     points for the proposed "closed" conformation of the enzyme. The
     polymerase also possesses a tunnel, which starts at the active site and
     terminates on the back surface of the enzyme. This tunnel of 19 ANG
     contains five basic amino acids, which may be engaged in NTP trafficking.
     In the present study, we exploited the crystal structure of the enzyme to
     elucidate the involvement of these two structural motifs in enzyme
     activity by site-directed mutagenesis. As predicted, the replacement of
     leucine 30 located in the A1-loop is detrimental to the NS5B activity.
     Heparin-Sepharose column chromatography and analytical ultracentrifugation
     experiments strongly suggest a local alteration in the structure of the
     Leu-30 mutant. An analysis of amino acid substitutions in Arg-222 and
     Lys-151 within the putative NTP tunnel indicates that Arg-222 was critical
     in delivering NTPs to the active site, whereas Lys-151 was dispensable.
     Interestingly, the substitution of lysine 151 for a glutamic acid resulted
     in an enzyme that was consistently more active in de novo synthesis as
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well as by "copy-back" mechanism of a self-primed substrate when compared with the wild type NS5B enzyme. Burst kinetic analyses indicate that the gain in function of K151E enzyme was primarily the result of the formation of more productive pre-initiation complexes that were used for the elongation reaction. In contrast to the recent observations, both the wild type and mutant enzymes were monomeric in solution, whereas molecules of higher order were apparent in the presence of RNA template.

L17 ANSWER 2 OF 10 BIOSIS COPYRIGHT 2003 BIOLOGICAL ABSTRACTS INC.
AN 2002:118688 BIOSIS
DN PREV200200118688
TI Functional properties of a monoclonal antibody inhibiting the hepatitis C virus **RNA-dependent RNA polymerase**
.
AU Moradpour, Darius; Bieck, Elke; Huegle, Thomas; Wels, Winfried; Wu, Jim Zhen; Hong, Zhi; Blum, Hubert E. (1); Bartenschlager, Ralf
CS (1) Dept. of Medicine II, University Hospital Freiburg, Hugstetter Str. 55, D-79106, Freiburg: heblum@ukl.uni-freiburg.de Germany
SO Journal of Biological Chemistry, (January 4, 2002) Vol. 277, No. 1, pp. 593-601. http://www.jbc.org/. print.
ISSN: 0021-9258.
DT Article
LA English
AB The hepatitis C virus (HCV) **RNA-dependent RNA polymerase** (RdRp), represented by nonstructural protein 5B (NS5B), has recently emerged as a promising target for antiviral intervention. Here, we describe the isolation, functional characterization, and molecular cloning of a monoclonal antibody (mAb) inhibiting the HCV RdRp. This mAb, designated 5B-12B7, binds with high affinity to a conformational epitope in the palm subdomain of the HCV RdRp and recognizes native NS5B expressed in the context of the entire HCV polyprotein or subgenomic replicons. Complete inhibition of RdRp activity in vitro was observed at equimolar concentrations of NS5B and mAb 5B-12B7, whereas RdRp activities of classical swine fever virus NS5B and **poliovirus** 3D polymerase were not affected. mAb 5B-12B7 selectively inhibited NTP binding to HCV NS5B, whereas binding of template RNA was unaffected, thus explaining the mechanism of action at the molecular level. The mAb 5B-12B7 heavy and light chain variable domains were cloned by **reverse** transcription-PCR, and a single chain Fv fragment was assembled for expression in Escherichia coli and in eukaryotic cells. The mAb 5B-12B7 single chain Fv fragment bound to NS5B both in vitro and in transfected human cell lines and therefore may be potentially useful for intracellular immunization against HCV. More important, detailed knowledge of the mAb 5B-12B7 contact sites on the enzyme may facilitate the development of small molecule RdRp inhibitors as novel antiviral agents.

L17 ANSWER 3 OF 10 BIOSIS COPYRIGHT 2003 BIOLOGICAL ABSTRACTS INC.
AN 2001:231971 BIOSIS
DN PREV200100231971
TI Determination of the mutation rate of **poliovirus RNA-dependent RNA polymerase**.
AU Wells, Virgen Rodriguez; Plotch, Stephen J.; DeStefano, Jeffrey J. (1)
CS (1) Department of Cell Biology and Molecular Genetics, University of Maryland College Park, Building 231, College Park, MD, 20742: jd146@umail.umd.edu USA
SO Virus Research, (April, 2001) Vol. 74, No. 1-2, pp. 119-132. print.
ISSN: 0168-1702.
DT Article
LA English
SL English
AB The fidelity of **poliovirus RNA-dependent RNA polymerase** (3Dpol) was determined using a system based on the fidelity of synthesis of the alpha-lac gene which codes for a subunit of beta-galactosidase. Synthesis products are screened for

mutations by an alpha-complementation assay, in which the protein product from alpha-lac is used in trans to complement beta-galactosidase activity in bacteria that do not express alpha-Lac. Several polymerases have been analyzed by this approach allowing comparisons to be drawn. The assay included RNA synthesis by 3Dpol on an RNA template that coded for the N-terminal region of alpha-Lac. The product of this reaction was used as a template for a second round of 3Dpol synthesis and the resulting RNA was **reverse** transcribed to DNA by MMLV-RT. The DNA was amplified by PCR and inserted into a vector used to transform Escherichia coli. The bacteria were screened for beta-galactosidase activity by blue-white phenotype analysis with white or faint blue colonies scored as errors made during synthesis on alpha-lac. Results showed a mutation rate for 3Dpol corresponding to apprxeq 4.5 X 10-4 errors per base (one error in apprxeq 2200 bases). Analysis of mutations showed that base substitutions occurred with greater frequency than deletions and insertions.

L17 ANSWER 4 OF 10 BIOSIS COPYRIGHT 2003 BIOLOGICAL ABSTRACTS INC.
AN 1999:86426 BIOSIS
DN PREV199900086426
TI Analysis of **RNA-dependent RNA** **polymerase** structure and function as guided by known polymerase structures and computer predictions of secondary structure.
AU O'Reilly, Erin K.; Kao, C. Cheng (1)
CS (1) Dep. Biol., Indiana Univ., Bloomington, ON 47405 USA
SO Virology, (Dec. 20, 1998) Vol. 252, No. 2, pp. 287-303. ISSN: 0042-6822.
DT General Review
LA English
AB RNA-dependent RNA polymerases (RdRps) function as the catalytic subunit of the viral replicase required for the replication of all positive strand RNA viruses. The vast majority of RdRps have been identified solely on the basis of sequence similarity. Structural studies of RdRps have lagged behind those of the DNA-dependent DNA polymerases, DNA-dependent RNA polymerases, and **reverse** transcriptases until the recent report of the partial crystal structure of the **poliovirus** RdRp, 3Dpol (Hansen, J. L., et al. (1997). Structure 5, 1109-1122). We seek to address whether all RdRps will have structures similar to those found in the **poliovirus** polymerase structure. Therefore, the PHD method of Rost and Sander (Rost, B., and Sander, C. (1993a). J. Mol. Biol. 232, 584-599; Rost, B., and Sander, C. (1994). Protein 19, 55-77) was used to predict the secondary structure of the RdRps from six different viral families: bromoviruses, tobamoviruses, tombusvirus, leviviruses, hepatitis C-like viruses, and picornaviruses. These predictions were compared with the known crystal structure of the **poliovirus** polymerase. The PHD method was also used to predict picornavirus structures in places in which the **poliovirus** crystal structure was disordered. All five families and the picornaviruses share a similar order of secondary structure elements present in their polymerase proteins. All except the leviviruses have the unique region observed in the **poliovirus** 3Dpol that is suggested to be involved in polymerase oligomerization. These structural predictions are used to explain the phenotypes of a collection of mutations that exist in several RNA polymerases. This analysis will help to guide further characterization of RdRps.

L17 ANSWER 5 OF 10 BIOSIS COPYRIGHT 2003 BIOLOGICAL ABSTRACTS INC.
AN 1997:453261 BIOSIS
DN PREV199799752464
TI One of two NTP binding sites in **poliovirus** RNA polymerase required for RNA replication.
AU Richards, Oliver C. (1); Ehrenfeld, Ellie
CS (1) Dep. Mol. Biol. Biochem., 3205 Biological Sci. II, Univ. Calif., Irvine, CA 92697 USA
SO Journal of Biological Chemistry, (1997) Vol. 272, No. 37, pp. 23261-23264. ISSN: 0021-9258.

DT Article
LA English
AB The **poliovirus RNA-dependent RNA polymerase** (3D-pol) has been shown to contain two NTP binding sites by chemical cross-linking of oxidized nucleotide to the intact protein. Only one site (Lys-61) was shown to be essential for RNA chain elongation activity by purified enzyme; however, a full-length viral RNA, coding for an altered lysine residue (K276L) in the second site, generated virus with a minute plaque phenotype that rapidly **reverted** to a wild-type phenotype with Arg-276 replacing Leu-276 in 3D. Viruses with lysine to leucine substitutions in other positions of the second binding site of their polymerase proteins grew with wild-type phenotype. To test the significance of the second binding site, **poliovirus** 3D-pol was generated with lysine (wild-type), leucine, or arginine at residue 276 and tested for NTP cross-linking using 32P-oxidized GTP. Analysis of cyanogen bromide peptides of each 3D preparation showed that the second NTP binding site had severely reduced NTP binding in mu-276(Leu) but not in the **revertant** mu-276(Arg), despite the reported requirement for lysine in the cross-linking reaction. To eliminate the possibility that 32P-oxidized GTP cross-linked to Arg at residue 276, a model system was designed with unmodified amino acid or acetylated (alpha-amino) amino acid and 32P-oxidized GTP. Cross-linking to lysine, but not leucine or arginine, was observed thus eliminating the possibility that NTP could be cross-linked to residue 276 in 3D. We conclude that NTP binding at the second site in **poliovirus** 3D is at lysine residues at positions other than 276 (278 or 283), and nucleotide binding at these sites has no bearing on elongation activity or replication of the virus. Nucleotide binding only at the site including Lys-61 is essential for RNA replication.

L17 ANSWER 6 OF 10 BIOSIS COPYRIGHT 2003 BIOLOGICAL ABSTRACTS INC.
AN 1997:452232 BIOSIS
DN PREV199799751435
TI Structure of the **RNA-dependent RNA polymerase** of **poliovirus**.
AU Hansen, Jeffrey L.; Long, Alexander M.; Schultz, Steve C. (1)
CS (1) Campus Box 215, Dep. Chemistry Biochemistry, Univ. Colorado, Boulder, CO 80309 USA
SO Structure (London), (1997) Vol. 5, No. 8, pp. 1109-1122.
ISSN: 0969-2126.
DT Article
LA English
AB Background: The central player in the replication of RNA viruses is the viral **RNA-dependent RNA polymerase**. The 53 kDa **poliovirus** polymerase, together with other viral and possibly host proteins, carries out viral RNA replication in the host cell cytoplasm. RNA-dependent RNA polymerases comprise a distinct category of polymerases that have limited sequence similarity to **reverse** transcriptases (RNA-dependent DNA polymerases) and perhaps also to DNA-dependent polymerases. Previously reported structures of RNA-dependent DNA polymerases, DNA-dependent DNA polymerases and a DNA-dependent RNA polymerase show that structural and evolutionary relationships exist between the different polymerase categories. Results: We have determined the structure of the **RNA-dependent RNA polymerase** of **poliovirus** at 2.6 ANG resolution by X-ray crystallography. It has the same overall shape as other polymerases, commonly described by analogy to a right hand. The structures of the 'fingers' and 'thumb' subdomains of **poliovirus** polymerase differ from those of other polymerases, but the palm subdomain contains a core structure very similar to that of other polymerases. This conserved core structure is composed of four of the amino acid sequence motifs described for RNA-dependent polymerases. Structure-based alignments of these motifs has enabled us to modify and extend previous sequence and structural alignments so as to relate sequence conservation to function. Extensive

regions of polymerase-polymerase interactions observed in the crystals suggest an unusual higher order structure that we believe is important for polymerase function. Conclusions: As a first example of a structure of an **RNA-dependent RNA polymerase**, the **poliovirus** polymerase structure provides for a better understanding of polymerase structure, function and evolution. In addition, it has yielded insights into an unusual higher order structure that may be critical for **poliovirus** polymerase function.

L17 ANSWER 7 OF 10 BIOSIS COPYRIGHT 2003 BIOLOGICAL ABSTRACTS INC.
AN 1997:295324 BIOSIS
DN PREV199799594527
TI **Poliovirus** RNA recombination in cell-free extracts.
AU Tang, Roderick S.; Barton, David J.; Flanegan, James B.; Kirkegaard, Karla (1)
CS (1) Dep. Microbiol. Immunol., Stanford Univ. Sch. Med., Stanford, CA 94305-5402 USA
SO RNA (New York), (1997) Vol. 3, No. 6, pp. 624-633.
ISSN: 1355-8382.
DT Article
LA English
AB **Poliovirus** RNA has been shown to undergo homologous genetic recombination at a high frequency In infected human cells. Recently it has become possible to mimic the entire intracellular replicative cycle of **poliovirus** replication In cytoplasmic extracts prepared from HeLa cells, resulting in the generation of infectious poliovirions. The mechanism of **poliovirus** RNA recombination has been shown previously to be coupled to RNA replication, presumably by template switching during the replication of parental RNAs. Experiments were designed to test whether recombinant **poliovirus** RNA molecules are produced in a cell-free environment. Recombinant molecules generated bear marker sequences that can be detected physically by **reverse** transcription and PCR. We report here successful detection of **poliovirus** RNA recombination In a cell-free replication system. The frequency measured for cell-free RNA recombination between two polymorphic marker loci 656 nt apart was between 10-2 and 10-3 recombinants/genome, a frequency comparable to or slightly higher than that measured for RNA recombination in Infected cells.

L17 ANSWER 8 OF 10 BIOSIS COPYRIGHT 2003 BIOLOGICAL ABSTRACTS INC.
AN 1996:20601 BIOSIS
DN PREV199698592736
TI An aspartic acid at amino acid 108 is required to rescue infectious virus after transfection of a **poliovirus** cDNA containing a CDGG but not SGDD amino acid motif in 3D-pol.
AU Walker, Donald E.; McPherson, David; Jablonski, Sandra A.; McPherson, Sylvia; Morrow, Casey D. (1)
CS (1) Dep. Microbiol., Univ. Alabama Birmingham, Birmingham, AL 35294 USA
SO Journal of Virology, (1995) Vol. 69, No. 12, pp. 8173-8177.
ISSN: 0022-538X.
DT Article
LA English
AB The **poliovirus RNA-dependent RNA polymerase** (3D-pol) contains a re-ion of homology centered around the amino acid motif YGDD (amino acids 326 to 329), which has been postulated to be involved in the catalytic activity of the enzyme. Previous studies from this laboratory have used oligonucleotide site-directed mutagenesis to substitute the tyrosine amino acid at this motif with other amino acids (S. A. Jablonski and C. D. Morrow, J. Virol. 67:373-381, 1993). The viruses recovered with 3D-pol genes with a methionine mutation also contained a second mutation at amino acid 108 resulting in a glutamic acid-to-aspartic acid change (3D-E-108 to 3D-D-108) in the **poliovirus** RNA polymerase. On the basis of these results, we suggested that the amino acid at position 108 might

interact with the YGDD region of the **poliovirus** polymerase. To further investigate this possibility, we have constructed a series of constructs in which the **poliovirus** RNA polymerases contained a mutation at amino acid 108 (3D-E-108 to 3D-D-108) as well as a mutation in which the tyrosine amino acid (3D-Y-326) was substituted with cysteine (3D-C-326) or serine (3D-S-326). The mutant 3D-pol polymerases were expressed in Escherichia coli, and in vitro enzyme activity was analyzed. Enzymes containing the 3D-D-108 mutation with the wild-type amino acid (3D-Y-326) demonstrated in vitro enzyme activity similar to that of the wild-type enzyme containing 3D-E-108. In contrast, enzymes with the 3D-C-326 or 3D-S-326 mutation had less in vitro activity than the wild type. The inclusion of the second mutation at amino acid 3D-D-108 did not significantly affect the in vitro activity of the polymerases containing 3D-C-326 or 3D-S-326 mutation. Transfections of **poliovirus** cDNAs containing the substitution at amino acid 326 with or without the second mutation at amino acid 108 were performed. Consistent with previous findings, we found that transfection of **poliovirus** cDNAs containing the 3D-C-326 or 3D-S-326 mutation in 3D-pol did not result in the production of virus. Surprisingly, transfection of the **poliovirus** cDNAs containing the 3D-D-108/C-326 double mutation, but not the 3D-D-108/S-326 mutation, resulted in the production of virus. The virus obtained from transfection of **poliovirus** cDNAs containing 3D-D-108/C-326 mutation replicated with kinetics similar to that of the wild-type virus. RNA sequence analysis of the region of the 3D-pol containing the 3D-C-326 mutation revealed that the codon for cysteine (UGC) **reverted** to the codon for tyrosine (UAC). The results of these studies establish that under the appropriate conditions, **poliovirus** has the capacity to **revert** mutations within the YGDD amino acid motif of the **poliovirus** 3D-pol gene and further strengthen the idea that interaction between amino acid 108 and the YGDD region of 3D-pol is required for viral replication.

L17 ANSWER 9 OF 10 BIOSIS COPYRIGHT 2003 BIOLOGICAL ABSTRACTS INC.
AN 1995:165379 BIOSIS
DN PREV199598179679
TI Mutation of the aspartic acid residues of the GDD sequence motif of **poliovirus RNA-dependent RNA polymerase** results in enzymes with altered metal ion requirements for activity.
AU Jablonski, Sandra A.; Morrow, Casey D. (1)
CS (1) Dep. Microbiol., Univ. Alabama Birmingham, Birmingham, AB 35294 USA
SO Journal of Virology, (1995) Vol. 69, No. 3, pp. 1532-1539.
ISSN: 0022-538X.
DT Article
LA English
AB The **poliovirus RNA-dependent RNA polymerase**, 3D-pol, is known to share a region of sequence homology with all RNA polymerases centered at the GDD amino acid motif. The two aspartic acids have been postulated to be involved in the catalytic activity and metal ion coordination of the enzyme. To test this hypothesis, we have utilized oligonucleotide site-directed mutagenesis to generate defined mutations in the aspartic acids of the GDD motif of the 3D-pol gene. The codon for the first aspartate (3D-D-328 (D refers to the single amino acid change, and the number refers to its position in the polymerase)) was changed to that for glutamic acid, histidine, asparagine, or glutamine; the codons for both aspartic acids were simultaneously changed to those for glutamic acids; and the codon for the second aspartic acid (3D-D-329) was changed to that for glutamic acid or asparagine. The mutant enzymes were expressed in Escherichia coli, and the in vitro poly(U) polymerase activity was characterized. All of the mutant 3D-pol enzymes were enzymatically inactive in vitro when tested over a range of Mg-2+ concentrations. However, when Mn-2+ was substituted for Mg-2+ in the in vitro assays, the mutant that substituted the second aspartic acid for asparagine (3D-N-329) was active. To further substantiate this finding, a

series of different transition metal ions were substituted for Mg-2+ in the poly(U) polymerase assay. The wild-type enzyme was active with all metals except Ca-2+, while the 3D-N-329 was active only when FeC-6H-7O-5 was used in the reaction. To determine the effects of the mutations on **poliovirus** replication, the mutant 3D-pol genes were subcloned into an infectious cDNA of **poliovirus**. The cDNAs containing the mutant 3D-pol genes did not produce infectious virus when transfected into tissue culture cells under standard conditions. Because of the activity of the 3D-N-329 mutant in the presence of Fe-2+ and Mn-2+, transfections were also performed in the presence of the different metal ions. Surprisingly, the transfection of the cDNA containing the 3D-N-329 mutation resulted in the production of virus at a low frequency in the presence of FeSO-4 or CoCl-2. The virus derived from transfection in the presence of FESO-4 grew slowly, while the viruses recovered from transfection in CoCl-2 grew at a rate which was similar to that of the wild-type **poliovirus**. The nucleotide sequence of the virus obtained from transfection in the presence of Co-2+ revealed that the 3D-N-329 mutation in the polymerase had **reverted** to a 3D-D-329. These results demonstrate that although the first aspartic acid residue is absolutely required for enzyme function, flexibility exists with respect to the requirement for the second aspartic acid residue. The activity of the 3D-N-329 mutant in the presence of different metal ions suggests the involvement of the aspartic acids in metal ion coordination during polymerization.

L17 ANSWER 10 OF 10 BIOSIS COPYRIGHT 2003 BIOLOGICAL ABSTRACTS INC.
AN 1993:319287 BIOSIS
DN PREV199396027637
TI RNA duplex unwinding activity of **poliovirus RNA-dependent RNA polymerase** 3D-pol.
AU Cho, Michael W. (1); Richards, Oliver C.; Dmitrieva, Tatiana M.; Agol, Vadim; Ehrenfeld, Ellie
CS (1) Dep. Molecular Biol. Biochem., Univ. California, Irvine, Irvine, CA 92717 USA
SO Journal of Virology, (1993) Vol. 67, No. 6, pp. 3010-3018.
ISSN: 0022-538X.
DT Article
LA English
AB The ability of highly purified preparations of **poliovirus RNA-dependent RNA polymerase**, 3D-pol, to unwind RNA duplex structures was examined during a chain elongation reaction in vitro. Using an antisense RNA prehybridized to an RNA template, we show that **poliovirus** polymerase can elongate through a highly stable RNA duplex of over 1,000 bp. Radiolabeled antisense RNA was displaced from the template during the reaction, and product RNAs which were equal in length to the template strand were synthesized. Unwinding did not occur in the absence of chain elongation and did not require hydrolysis of the gamma-phosphate of ATP. The rate of elongation through the duplex region was comparable to the rate of elongation on the single-stranded region of the template. Parallel experiments conducted with avian myeloblastosis virus **reverse** transcriptase showed that this enzyme was not able to unwind the RNA duplex, suggesting that strand displacement by **poliovirus** 3D-pol is not a property shared by all polymerases.

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=> s reversion
L20      18062 REVERSION

=> s l19 and l20
L21         22 L19 AND L20

=> d l21 1-22 bib, ab

L21  ANSWER 1 OF 22  USPATFULL
AN     2002:259414  USPATFULL
TI     Methods of inducing mucosal immunity
IN     Weiner, David B., Merion, PA, UNITED STATES
       Wang, Bin, Havertown, PA, UNITED STATES
       Ugen, Kenneth E., Philadelphia, PA, UNITED STATES
PA     The trustees of the University of Pennsylvania (U.S. corporation)
PI     US 2002142987      A1   20021003
AI     US 2002-76900      A1   20020214 (10)
RLI    Continuation of Ser. No. US 1994-357398, filed on 16 Dec 1994, GRANTED,
       Pat. No. US 6348449
DT     Utility
FS     APPLICATION
LREP   Woodcock Washburn LLP, One Liberty Place - 46th Floor, Philadelphia, PA,
       19103
CLMN   Number of Claims: 14
ECL    Exemplary Claim: 1
DRWN   2 Drawing Page(s)
LN.CNT 2388
CAS INDEXING IS AVAILABLE FOR THIS PATENT.
AB     Methods of inducing mucosal immunity in individuals against proteins and
       peptides are disclosed. The methods comprise the step of administering
       topically or by lavage into mucosal tissue selected from the group
       consisting of rectal, vaginal, urethral, sublingual and buccal, a
       nucleic acid molecule that comprises a nucleotide sequence that encodes
       a protein or peptide that comprises an epitope against which mucosal
       immunity is desired. The methods may be used to immunize and individual
       against a pathogen infection, hyperproliferative diseases or autoimmune
       diseases using nucleic acid molecules which encode proteins and peptides
       that share an epitope with a pathogen antigen or protein associated with
       cells involved in hyperproliferative diseases or autoimmune diseases,
       respectively,

L21  ANSWER 2 OF 22  USPATFULL
AN     2002:252908  USPATFULL
TI     Multiple component RNA vector system for expression of foreign sequences
IN     Lewandowski, Dennis J., Auburndale, FL, UNITED STATES
       Dawson, William O., Winter Haven, FL, UNITED STATES
       Turpen, Thomas H., Vacaville, CA, UNITED STATES
       Pogue, Gregory P., Vacaville, CA, UNITED STATES
PI     US 2002138873      A1   20020926
AI     US 2002-57335      A1   20020124 (10)
RLI    Continuation of Ser. No. US 1999-265575, filed on 9 Mar 1999, PENDING
DT     Utility
FS     APPLICATION
LREP   HOWREY SIMON ARNOLD & WHITE, LLP, BOX 34, 301 RAVENSWOOD AVE., MENLO
       PARK, CA, 94025
CLMN   Number of Claims: 43
ECL    Exemplary Claim: 1
DRWN   8 Drawing Page(s)
LN.CNT 1292
CAS INDEXING IS AVAILABLE FOR THIS PATENT.
AB     The present invention features a multiple component RNA vector system,
       which consists of RNA virus-derived RNA replicons and helper viruses.
       The present invention further features a method for producing foreign
       RNAs, effector RNAs, proteins or peptides in plants using the multiple
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component RNA vector system. Moreover, the present invention provides a method for stable and systemic production of foreign RNAs, effector RNAs, proteins and peptides using the multiple component RNA vector system.

L21 ANSWER 3 OF 22 USPATFULL
AN 2002:238656 USPATFULL
TI Recombinant newcastle disease virus RNA expression systems and vaccines
IN Garcia-Sastre, Adolfo, New York, NY, United States
Palese, Peter, Leonia, NJ, United States
PA Mount Sinai School of Medicine of New York University, New York, NY, United States (U.S. corporation)
PI US 6451323 B1 20020917
AI US 2000-576567 20000522 (9)
RLI Continuation-in-part of Ser. No. US 1998-152845, filed on 14 Sep 1998, now patented, Pat. No. US 6146642
DT Utility
FS GRANTED
EXNAM Primary Examiner: Park, Hankyel T.
LREP Pennie & Edmonds LLP
CLMN Number of Claims: 126
ECL Exemplary Claim: 1
DRWN 11 Drawing Figure(s); 11 Drawing Page(s)
LN.CNT 1744
CAS INDEXING IS AVAILABLE FOR THIS PATENT.
AB This invention relates to genetically engineered Newcastle disease viruses and viral vectors which express heterologous genes or mutated Newcastle disease viral genes or a combination of viral genes derived from different strains of Newcastle disease virus. The invention relates to the construction and use of recombinant negative strand NDV viral RNA templates which may be used with viral RNA-directed RNA polymerase to express heterologous gene products in appropriate host cells and/or to rescue the heterologous gene in virus particles. In a specific embodiment of the invention, the heterologous gene product is a peptide or protein derived from the genome of a human immunodeficiency virus. The RNA templates of the present invention may be prepared by transcription of appropriate DNA sequences using any DNA-directed RNA polymerase such as bacteriophage T7, T3, SP6 polymerase, or eukaryotic polymerase I.

L21 ANSWER 4 OF 22 USPATFULL
AN 2002:34422 USPATFULL
TI Methods of inducing mucosal immunity
IN Weiner, David B., Merion, PA, United States
Wang, Bin, Havertown, PA, United States
Ugen, Kenneth E., Philadelphia, PA, United States
PA The Trustees of the University of Pennsylvania, Philadelphia, PA, United States (U.S. corporation)
PI US 6348449 B1 20020219
AI US 1994-357398 19941216 (8)
RLI Continuation-in-part of Ser. No. US 1993-125012, filed on 21 Sep 1993, now patented, Pat. No. US 5593972, issued on 14 Jan 1996
DT Utility
FS GRANTED
EXNAM Primary Examiner: Crouch, Deborah
LREP Woodcock Washburn , LLP
CLMN Number of Claims: 9
ECL Exemplary Claim: 1
DRWN 8 Drawing Figure(s); 2 Drawing Page(s)
LN.CNT 2479
CAS INDEXING IS AVAILABLE FOR THIS PATENT.
AB Methods of inducing mucosal immunity in individuals against proteins and peptides are disclosed. The methods comprise the step of administering topically or by lavage into mucosal tissue selected from the group

consisting of rectal, vaginal, urethral, sublingual and buccal, a nucleic acid molecule that comprises a nucleotide sequence that encodes a protein or peptide that comprises an epitope against which mucosal immunity is desired. The methods may be used to immunize an individual against a pathogen infection, hyperproliferative diseases or autoimmune diseases using nucleic acid molecules which encode proteins and peptides that share an epitope with a pathogen antigen or protein associated with cells involved in hyperproliferative diseases or autoimmune diseases, respectively.

L21 ANSWER 5 OF 22 USPATFULL
AN 2001:130869 USPATFULL
TI Method for generating nonpathogenic infectious pancreatic necrosis virus (IPNV) from synthetic RNA transcripts
IN Vakharia, Vikram N., Bowie, MD, United States
Yao, Kun, College Park, MD, United States
PA University of Maryland-Biotechnology Institute, College Park, MD, United States (U.S. corporation)
PI US 6274147 B1 20010814
AI US 1999-282147 19990331 (9)
PRAI US 1998-80178P 19980331 (60)
DT Utility
FS GRANTED
EXNAM Primary Examiner: Mosher, Mary E.
LREP Arent Fox Plotkin Kintner Kahn PLLC.
CLMN Number of Claims: 24
ECL Exemplary Claim: 1
DRWN 12 Drawing Figure(s); 12 Drawing Page(s)
LN.CNT 1615
CAS INDEXING IS AVAILABLE FOR THIS PATENT.
AB A system for the generation of live, nonpathogenic infectious pancreatic necrosis virus (IPNV), a segmented double-stranded (ds)RNA virus of the Birnavirdae family, using synthetic transcripts derived from cloned DNA has been developed. Independent full-length cDNA clones were constructed which contained the coding and non-coding regions of RNA segments A and B of IPNV, respectively. Segment A was modified to prevent the expression of NS protein. Synthetic RNAs of both segments were produced by in vitro transcription of linearized plasmids with T7 RNA polymerase. Transfection of CHSE cells with combined plus-sense transcripts of both segments generated infectious virus. The development of a system for producing NS protein deficient IPNV will greatly facilitate studies of viral pathogenesis, and the development of live attenuated vaccines for IPNV.

L21 ANSWER 6 OF 22 USPATFULL
AN 2001:71104 USPATFULL
TI Method for generating nonpathogenic infections birnavirus from synthetic RNA transcripts
IN Vakharia, Vikram N., Bowie, MD, United States
Yao, Kun, College Park, MD, United States
PA University of Maryland-Biotechnology Institute, College Park, MD, United States (U.S. corporation)
PI US 6231868 B1 20010515
AI US 1997-940968 19970930 (8)
DT Utility
FS Granted
EXNAM Primary Examiner: Mosher, Mary E.
LREP Arent Fox Kintner Plotkin & Kahn, PLLC
CLMN Number of Claims: 20
ECL Exemplary Claim: 1
DRWN 30 Drawing Figure(s); 14 Drawing Page(s)
LN.CNT 1344
CAS INDEXING IS AVAILABLE FOR THIS PATENT.
AB A system for the generation of live, nonpathogenic Birnavirus such as

infectious bursal disease virus (IBDV), a segmented double-stranded (ds)RNA virus of the Birnavirdae family, using synthetic transcripts derived from cloned DNA has been developed. Independent full-length cDNA clones were constructed which contained the coding and non-coding regions of RNA segments A and B of IBDV, respectively. Segment A was modified to prevent the expression of NS protein. Synthetic RNAs of both segments were produced by in vitro transcription of linearized plasmids with T7 RNA polymerase. Transfection of Vero cells with combined plus-sense transcripts of both segments generated infectious virus as early as 36 hours post-transfection. The development of a system for producing NS protein deficient IBDV will greatly facilitate studies of immunosuppression, and aid in the development of live attenuated vaccines for IBDV.

L21 ANSWER 7 OF 22 USPATFULL
AN 2001:33252 USPATFULL
TI Compositions and methods for delivery of genetic material
IN Carrano, Richard A., Paoli, PA, United States
Wang, Bin, Haidian, China
Weiner, David B., Merion, PA, United States
PA The Trustees of the University of Pennsylvania, Philadelphia, PA, United States (U.S. corporation)
Apollan, Inc., Malvern, PA, United States (U.S. corporation)
PI US 6197755 B1 20010306
AI US 1999-321461 19990527 (9)
RLI Continuation of Ser. No. US 704701, now patented, Pat. No. US 5962428
Continuation of Ser. No. US 1994-221579, filed on 1 Apr 1994, now patented, Pat. No. US 5739118, issued on 14 Apr 1998
DT Utility
FS Granted
EXNAM Primary Examiner: Schwartzman, Robert A.
LREP Woodcock Washburn Kurtz Mackiewicz & Norris LLP
CLMN Number of Claims: 24
ECL Exemplary Claim: 1
DRWN 6 Drawing Figure(s); 5 Drawing Page(s)
LN.CNT 3329
CAS INDEXING IS AVAILABLE FOR THIS PATENT.
AB Methods of introducing genetic material into cells of an individual and compositions and kits for practicing the same are disclosed. The methods comprise the steps of contacting cells of an individual with a genetic vaccine facilitator and administering to the cells, a nucleic acid molecule that is free of retroviral particles. The nucleic acid molecule comprises a nucleotide sequence that encodes a protein that comprises at least one epitope that is identical or substantially similar to an epitope of a pathogen antigen or an antigen associated with a hyperproliferative or autoimmune disease, a protein otherwise missing from the individual due to a missing, non-functional or partially functioning gene, or a protein that produce a therapeutic effect on an individual. Methods of prophylactically and therapeutically immunizing an individual against HIV are disclosed. Pharmaceutical compositions and kits for practicing methods of the present invention are disclosed.

L21 ANSWER 8 OF 22 USPATFULL
AN 2001:1631 USPATFULL
TI Methods for making modified recombinant vesiculoviruses
IN Rose, John K., Guilford, CT, United States
PA Yale University, New Haven, CT, United States (U.S. corporation)
PI US 6168943 B1 20010102
AI US 1996-646695 19960503 (8)
RLI Continuation-in-part of Ser. No. US 1995-435032, filed on 4 May 1995
DT Utility
FS Granted
EXNAM Primary Examiner: Bui, Phuong T.
LREP Pennie & Edmonds LLP

CLMN Number of Claims: 13
ECL Exemplary Claim: 1
DRWN 55 Drawing Figure(s); 55 Drawing Page(s)
LN.CNT 2933
CAS INDEXING IS AVAILABLE FOR THIS PATENT.
AB The invention provides recombinant replicable vesiculoviruses. The invention provides a method which, for the first time, successfully allows the production and recovery of replicable vesiculoviruses, as well as recombinant replicable vesiculoviruses, from cloned DNA, by a method comprising expression of the full-length positive-strand vesiculovirus antigenomic RNA in host cells. The recombinant vesiculoviruses do not cause serious pathology in humans, can be obtained in high titers, and have use as vaccines. The recombinant vesiculoviruses can also be inactivated for use as killed vaccines.

L21 ANSWER 9 OF 22 USPATFULL
AN 2000:153278 USPATFULL
TI Recombinant new castle disease virus RNA expression systems and vaccines
IN Garcia-Sastre, Adolfo, New York, NY, United States
Palese, Peter, Leonia, NJ, United States
PA Mount Sinai School of Medicine, of the City University of New York, New York, NY, United States (U.S. corporation)
PI US 6146642 20001114
AI US 1998-152845 19980914 (9)
DT Utility
FS Granted
EXNAM Primary Examiner: Park, Hankyel
LREP Pennie & Edmonds LLP
CLMN Number of Claims: 14
ECL Exemplary Claim: 1
DRWN 8 Drawing Figure(s); 8 Drawing Page(s)
LN.CNT 1175
CAS INDEXING IS AVAILABLE FOR THIS PATENT.
AB This invention relates to genetically engineered Newcastle disease viruses and viral vectors which express heterologous genes or mutated Newcastle disease viral genes or a combination of viral genes derived from different strains of Newcastle disease virus. The invention relates to the construction and use of recombinant negative strand NDV viral RNA templates which may be used with viral RNA-directed RNA polymerase to express heterologous gene products in appropriate host cells and/or to rescue the heterologous gene in virus particles. In a specific embodiment of the invention, the heterologous gene product is a peptide or protein derived from the genome of a human immunodeficiency virus. The RNA templates of the present invention may be prepared by transcription of appropriate DNA sequences using a DNA-directed RNA polymerase such as bacteriophage T7, T3 or the SP6 polymerase.

L21 ANSWER 10 OF 22 USPATFULL
AN 2000:113486 USPATFULL
TI Live attenuated vaccines based on cp45 HPIV-3 strain and method to ensure attenuation in such vaccines
IN Belshe, Robert B., St. Louis, MO, United States
Ray, Ranjit, St. Louis, MO, United States
PA St. Louis University, St. Louis, MO, United States (U.S. corporation)
PI US 6110457 20000829
AI US 1997-987439 19971209 (8)
RLI Continuation-in-part of Ser. No. US 1995-569853, filed on 8 Dec 1995, now patented, Pat. No. US 5869036, issued on 9 Feb 1999
PRAI US 1996-32943P 19961209 (60)
DT Utility
FS Granted
EXNAM Primary Examiner: Clark, Deborah J.
LREP Senniger, Powers, Leavitt & Roedel
CLMN Number of Claims: 66

ECL Exemplary Claim: 1,2
DRWN 28 Drawing Figure(s); 16 Drawing Page(s)
LN.CNT 2745
CAS INDEXING IS AVAILABLE FOR THIS PATENT.
AB The present invention is based upon correlation of two attenuating lesions of the cp45 strain to specific genetic defects in the viral genome of cp45. Specifically, it is now understood that a significant level of attenuation of cp45 giving rise to its temperature-sensitive and cold-adapted phenotypes is directly associated with **mutation** of the large, or L, gene of cp45 relative to the corresponding gene in the wild-type JS strain. Moreover, it is further understood that a second attenuating lesion exits independent of the temperature-sensitive lesion, and is directly associated with **mutation** of the hemagglutinin-neuraminidase gene, or HN gene, of cp45 relative to the corresponding gene in the wild-type HPIV-3 (JS) strain. The correlation of these two attenuating lesions of cp45 to specific genes enables several practical applications. It is now possible to create vaccines directed at other wild-type HPIV-3 viruses and, additionally, vaccines directed at target viruses other than HPIV-3 using genetic engineering techniques. For example, the mutated L and/or HN genes of cp45 can be incorporated into the viral genome of a target virus. Alternatively, the genes of the target virus which encode its surface antigens can be incorporated into the viral genome of cp45. Moreover, it is possible to determine whether an HPIV-3 strain or a hybrid virus strain made by the methods disclosed herein is attenuated by confirming the presence or absence of mutations in its L and/or HN genes.

L21 ANSWER 11 OF 22 USPATFULL
AN 1999:163489 USPATFULL
TI Recombinant negative strand RNA viruses
IN Palese, Peter, 414 Highwood Ave., Leonia, NJ, United States 07605
Garcia-Sastre, Adolfo, 1249 Park Ave., #8D, New York, NY, United States 10029
PI US 6001634 19991214
AI US 1998-106377 19980629 (9)
RLI Division of Ser. No. US 1994-252508, filed on 1 Jun 1994, now patented, Pat. No. US 5854037, issued on 29 Dec 1998 which is a continuation-in-part of Ser. No. US 1994-190698, filed on 1 Feb 1994, now abandoned which is a continuation of Ser. No. US 1992-925061, filed on 4 Aug 1992, now abandoned which is a division of Ser. No. US 1990-527237, filed on 22 May 1990, now patented, Pat. No. US 5166057, issued on 24 Nov 1992 which is a continuation-in-part of Ser. No. US 1989-440053, filed on 21 Nov 1989, now abandoned which is a continuation-in-part of Ser. No. US 1989-399728, filed on 28 Aug 1989, now abandoned
DT Utility
FS Granted
EXNAM Primary Examiner: McKelvey, Terry
LREP Pennie & Edmonds LLP
CLMN Number of Claims: 6
ECL Exemplary Claim: 1
DRWN 42 Drawing Figure(s); 26 Drawing Page(s)
LN.CNT 3516
CAS INDEXING IS AVAILABLE FOR THIS PATENT.
AB Recombinant negative-strand viral RNA templates are described which may be used with purified RNA-directed RNA polymerase complex to express heterologous gene products in appropriate host cells and/or to rescue the heterologous gene in virus particles. The RNA templates are prepared by transcription of appropriate DNA sequences with a DNA-directed RNA polymerase. The resulting RNA templates are of the negative-polarity and contain appropriate terminal sequences which enable the viral RNA-synthesizing apparatus to recognize the template. Bicistronic mRNAs can be constructed to permit internal initiation of translation of viral sequences and allow for the expression of foreign protein coding

sequences from the regular terminal initiation site, or vice versa.

L21 ANSWER 12 OF 22 USPATFULL
AN 1999:141912 USPATFULL
TI Compositions and methods for delivery of genetic material
IN Weiner, David B., Merion, PA, United States
Williams, William V., Havertown, PA, United States
Wang, Bin, Havertown, PA, United States
PA The Trustees of The University of Pennsylvania, Philadelphia, PA, United States (U.S. corporation)
The Wistar Institute, Philadelphia, PA, United States (U.S. corporation)
PI US 5981505 19991109
WO 9416737 19940804
AI US 1997-979385 19971126 (8)
WO 1994-US899 19940126
19950828 PCT 371 date
19950828 PCT 102(e) date
RLI Continuation-in-part of Ser. No. US 1993-124962, filed on 21 Sep 1993, now abandoned And a continuation-in-part of Ser. No. US 1993-93235, filed on 15 Jul 1993, now abandoned And a continuation of Ser. No. US 1995-495684, filed on 28 Aug 1995, now abandoned which is a continuation-in-part of Ser. No. US 1993-125012, filed on 21 Sep 1993, now patented, Pat. No. US 5593972, issued on 14 Jan 1997 which is a continuation-in-part of Ser. No. US 1993-29336, filed on 11 Mar 1993, now abandoned which is a continuation-in-part of Ser. No. US 1993-8342, filed on 26 Jan 1993, now abandoned
DT Utility
FS Granted
EXNAM Primary Examiner: Railey, II, Johnny F.
LREP Woodcock Washburn Kurtz Mackiewicz & Norris LLP
CLMN Number of Claims: 75
ECL Exemplary Claim: 1
DRWN 23 Drawing Figure(s); 12 Drawing Page(s)
LN.CNT 4084
CAS INDEXING IS AVAILABLE FOR THIS PATENT.
AB Methods of inducing genetic material into cells of an individual and compositions and kits for practicing the same are disclosed. The methods comprise the steps of contacting cells of an individual with a polynucleotide function enhancer and administering to the cells, a nucleic acid molecule that is free of retroviral particles. The nucleic acid molecule comprises a nucleotide sequence that encodes a protein that comprises at least one epitope that is identical or substantially similar to an epitope of a pathogen antigen or an antigen associated with a hyperproliferative or autoimmune disease, a protein otherwise missing from the individual due to a missing, non-functional or partially functioning gene, or a protein that produces a therapeutic effect on an individual. Methods of prophylactically and therapeutically immunizing an individual against HIV are disclosed. Pharmaceutical compositions and kits for practicing methods of the present invention are disclosed.

L21 ANSWER 13 OF 22 USPATFULL
AN 1999:121330 USPATFULL
TI Compositions and methods for delivery of genetic material
IN Carrano, Richard A., Paoli, PA, United States
Wang, Bin, Haidian, China
Weiner, David B., Merion, PA, United States
PA Apollon, Inc., Malvern, PA, United States (U.S. corporation)
The Trustees Of The University of Pennsylvania, Philadelphia, PA, United States (U.S. corporation)
PI US 5962428 19991005
WO 9526718 19951012
AI US 1996-704701 19960916 (8)
WO 1995-US4071 19950330

19960916 PCT 371 date
19960916 PCT 102(e) date
RLI Continuation of Ser. No. US 221579
DT Utility
FS Granted
EXNAM Primary Examiner: Elliott, George C.; Assistant Examiner: Schwartzman, Robert
LREP Woodcock Washburn Kurtz Mackiewcz & Norris LLP
CLMN Number of Claims: 42
ECL Exemplary Claim: 1
DRWN 6 Drawing Figure(s); 5 Drawing Page(s)
LN.CNT 3606
CAS INDEXING IS AVAILABLE FOR THIS PATENT.
AB Methods of introducing genetic material into cells of an individual and compositions and kits for practicing the same are disclosed. The methods comprise the steps of contacting cells of an individual with a genetic vaccine facilitator and administering to the cells a nucleic acid molecule that is free of retroviral particles. The nucleic acid molecule comprises a nucleotide sequence that encodes a protein that comprises at least one epitope that is identical or substantially similar to an epitope of a pathogen antigen or an antigen associated with a hyperproliferative or autoimmune disease, a protein otherwise missing from the individual due to a missing, non-functional or partially functioning gene, or a protein that produces a therapeutic effect on an individual. Methods of prophylactically and therapeutically immunizing an individual against HIV are disclosed. Pharmaceutical compositions and kits for practicing methods of the present invention are disclosed.

L21 ANSWER 14 OF 22 USPATFULL
AN 1999:18710 USPATFULL
TI Live attenuated vaccines based on CP45 HPIV-3 strain and method to ensure attenuation in such vaccine
IN Belshe, Robert B., St. Louis, MO, United States
Ray, Ranjit, St. Louis, MO, United States
PA St. Louis University, St. Louis, MO, United States (U.S. corporation)
PI US 5869036 19990209
AI US 1995-569853 19951208 (8)
DT Utility
FS Granted
EXNAM Primary Examiner: Chambers, Jasemine C.; Assistant Examiner: Clark, Deborah J. R.
LREP Senniger, Powers, Leavitt & Roedel
CLMN Number of Claims: 55
ECL Exemplary Claim: 1,4,17,32,43
DRWN 13 Drawing Figure(s); 6 Drawing Page(s)
LN.CNT 1842
CAS INDEXING IS AVAILABLE FOR THIS PATENT.
AB The present invention is based upon the observation that the temperature sensitive phenotype of the cp45 strain of HPIV-3 correlates to a **mutation** in the large, or L, gene of cp45 relative to the corresponding gene in the wild-type strain. This correlation enables new vaccines directed at viruses other than HPIV-3 by combining, through genetic engineering methods, the region of the cp45 viral genome which encodes proteins responsible for replication and internal structure with the region of the genome of the target virus which encodes proteins responsible for attachment, penetration and release of the virus and virus progeny, respectfully. Moreover, it is possible to determine whether HPIV-3 or a cp45-hybrid virus is attenuated by confirming the presence or absence of mutations in its L gene.

L21 ANSWER 15 OF 22 USPATFULL
AN 1998:162308 USPATFULL
TI Recombinant negative strand RNA virus expression systems and vaccines
IN Palese, Peter, Leonia, NJ, United States

Garcia-Sastre, Adolfo, New York, NY, United States
PA The Mount Sinai School of Medicine of the City University of New York, New York, NY, United States (U.S. corporation)
PI US 5854037 19981229
AI US 1994-252508 19940601 (8)
RLI Continuation-in-part of Ser. No. US 1994-190698, filed on 1 Feb 1994, now abandoned which is a continuation of Ser. No. US 1992-925061, filed on 4 Aug 1992, now abandoned which is a division of Ser. No. US 1990-527237, filed on 22 May 1990, now patented, Pat. No. US 5166057 which is a continuation-in-part of Ser. No. US 1989-440053, filed on 21 Nov 1989, now abandoned which is a continuation-in-part of Ser. No. US 1989-399728, filed on 28 Aug 1989, now abandoned
DT Utility
FS Granted
EXNAM Primary Examiner: Fleisher, Mindy; Assistant Examiner: McKelvey, Terry A.
LREP Pennie & Edmonds LLP
CLMN Number of Claims: 34
ECL Exemplary Claim: 1
DRWN 42 Drawing Figure(s); 26 Drawing Page(s)
LN.CNT 3706
CAS INDEXING IS AVAILABLE FOR THIS PATENT.
AB Recombinant negative-strand viral RNA templates are described which may be used with purified RNA-directed RNA polymerase complex to express heterologous gene products in appropriate host cells and/or to rescue the heterologous gene in virus particles. The RNA templates are prepared by transcription of appropriate DNA sequences with a DNA-directed RNA polymerase. The resulting RNA templates are of the negative-polarity and contain appropriate terminal sequences which enable the viral RNA-synthesizing apparatus to recognize the template. Bicistronic mRNAs can be constructed to permit internal initiation of translation of viral sequences and allow for the expression of foreign protein coding sequences from the regular terminal initiation site, or vice versa.

L21 ANSWER 16 OF 22 USPATFULL
AN 1998:147242 USPATFULL
TI Recombinant negative strand RNA virus expression systems
IN Clarke, David Kirkwood, Pacifica, CA, United States
Palese, Peter M., Leonia, NJ, United States
PA Aviron, Mountain View, CA, United States (U.S. corporation)
PI US 5840520 19981124
AI US 1994-316439 19940930 (8)
RLI Continuation-in-part of Ser. No. US 1994-190698, filed on 1 Feb 1994, now abandoned which is a continuation of Ser. No. US 1992-925061, filed on 4 Aug 1992, now abandoned which is a division of Ser. No. US 1990-527237, filed on 22 May 1990, now patented, Pat. No. US 5166057 which is a continuation-in-part of Ser. No. US 1989-440053, filed on 21 Nov 1989, now abandoned And Ser. No. US 1989-399728, filed on 28 Aug 1989, now abandoned
DT Utility
FS Granted
EXNAM Primary Examiner: Woodward, Michael P.; Assistant Examiner: Salimi, Ali R.
LREP Pennie & Edmonds LLP
CLMN Number of Claims: 9
ECL Exemplary Claim: 1
DRWN 34 Drawing Figure(s); 23 Drawing Page(s)
LN.CNT 3189
CAS INDEXING IS AVAILABLE FOR THIS PATENT.
AB Recombinant negative strand virus RNA templates which may be used to express heterologous gene products and/or to construct chimeric viruses are described. Influenza viral polymerase, which was prepared depleted of viral RNA, was used to copy small RNA templates prepared from plasmid-encoded sequences. Template constructions containing only the 3'

end of genomic RNA were shown to be efficiently copied, indicative that the promoter lay solely within the 15 nucleotide 3' terminus. Sequences not specific for the influenza viral termini were not copied, and, surprisingly, RNAs containing termini identical to those from plus sense cRNA were copied at low levels. The specificity for recognition of the virus-sense promoter was further defined by site-specific mutagenesis. It was also found that increased level of viral protein were required in order to catalyze both the cap-endonuclease primed and primer-free RNA synthesis from these model templates as well as from genomic length RNAs. This indicated that this reconstituted system had catalytic properties very similar to those of native viral RNPs. High levels of expression of a heterologous gene was obtained using the constructs and methods described. The system was exemplified using Influenza and respiratory syncytial virus.

L21 ANSWER 17 OF 22 USPATFULL
AN 1998:124205 USPATFULL
TI Recombinant negative strand RNA virus expression systems and vaccines
IN Palese, Peter, Leonia, NJ, United States
Garcia-Sastre, Adolfo, New York, NY, United States
PA The Mount Sinai School of Medicine of the City University of New York, New York, NY, United States (U.S. corporation)
PI US 5820871 19981013
AI US 1995-470887 19950606 (8)
RLI Division of Ser. No. US 1994-252508, filed on 1 Jun 1994 which is a continuation-in-part of Ser. No. US 1994-190698, filed on 1 Feb 1994, now abandoned which is a continuation of Ser. No. US 1992-925061, filed on 4 Aug 1992, now abandoned which is a division of Ser. No. US 1990-527237, filed on 22 May 1990, now patented, Pat. No. US 5166057 which is a continuation-in-part of Ser. No. US 1989-440053, filed on 21 Nov 1989, now abandoned which is a continuation-in-part of Ser. No. US 1989-399728, filed on 28 Aug 1989, now abandoned
DT Utility
FS Granted
EXNAM Primary Examiner: Fleisher, Mindy; Assistant Examiner: McKelvey, Terry A.
LREP Pennie & Edmonds LLP
CLMN Number of Claims: 17
ECL Exemplary Claim: 1
DRWN 42 Drawing Figure(s); 26 Drawing Page(s)
LN.CNT 3448
CAS INDEXING IS AVAILABLE FOR THIS PATENT.
AB Recombinant negative-strand viral RNA templates are described which may besed with purified RNA-directed RNA polymerase complex to express heterologous gene products in appropriate host cells and/or to rescue the heterologous gene in virus particles. The RNA templates are prepared by transcription of appropriate DNA sequences with a DNA-directed RNA polymerase. The resulting RNA templates are of the negative-polarity and contain appropriate terminal sequences which enable the viral RNA-synthesizing apparatus to recognize the template. Bicistronic mRNAs can be constructed to permit internal initiation of translation of viral sequences and allow for the expression of foreign protein coding sequences from the regular terminal initiation site, or vice versa.

L21 ANSWER 18 OF 22 USPATFULL
AN 1998:88690 USPATFULL
TI Recombinant negative strand RNA virus expression systems and vaccines
IN Palese, Peter, Leonia, NJ, United States
PA The Mount Sinai School of Medicine of the City University of New York, New York, NY, United States (U.S. corporation)
PI US 5786199 19980728
AI US 1994-323192 19941014 (8)
RLI Continuation-in-part of Ser. No. US 1994-252508, filed on 1 Jun 1994 which is a continuation-in-part of Ser. No. US 1994-190698, filed on 1

Feb 1994, now abandoned which is a continuation-in-part of Ser. No. US 1992-925061, filed on 4 Aug 1992, now abandoned which is a division of Ser. No. US 1990-527237, filed on 22 May 1990, now patented, Pat. No. US 5166057 which is a continuation-in-part of Ser. No. US 1989-440053, filed on 21 Nov 1989, now abandoned which is a continuation-in-part of Ser. No. US 1989-399728, filed on 28 Aug 1989, now abandoned

DT Utility
FS Granted
EXNAM Primary Examiner: Degen, Nancy; Assistant Examiner: McKelvey, Terry A.
LREP Pennie & Edmonds LLP
CLMN Number of Claims: 17
ECL Exemplary Claim: 1
DRWN 53 Drawing Figure(s); 32 Drawing Page(s)
LN.CNT 4303
CAS INDEXING IS AVAILABLE FOR THIS PATENT.

AB Recombinant negative-strand viral RNA templates are described which may be used with purified RNA-directed RNA polymerase complex to express heterologous gene products in appropriate host cells and/or to rescue the heterologous gene in virus particles. Heterologous gene products include peptides or proteins derived from HIV which may be presented by a chimeric influenza virus to generate an immune response that is protective against challenge with HIV. A chimeric virus is described which contains an HIV peptide inserted into an influenza protein and which induced both humoral and cell-mediated immune responses against HIV. The RNA templates are prepared by transcription of appropriate DNA sequences with a DNA-directed RNA polymerase. The resulting RNA templates are of the negative-polarity and contain appropriate terminal sequences which enable the viral RNA-synthesizing apparatus to recognize the template.

L21 ANSWER 19 OF 22 USPATFULL
AN 1998:39510 USPATFULL
TI Compositions and methods for delivery of genetic material
IN Carrano, Richard A., Paoli, PA, United States
Wang, Bin, Beijing, China
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PA Apollon, Inc., Malvern, PA, United States (U.S. corporation)
The Trustees of the University of Pennsylvania, Philadelphia, PA, United States (U.S. corporation)
PI US 5739118 19980414
AI US 1994-221579 19940401 (8)
DT Utility
FS Granted
EXNAM Primary Examiner: Rories, Charles C. P.
LREP Woodcock Washburn Kurtz Mackiewicz & Norris, LLP
CLMN Number of Claims: 23
ECL Exemplary Claim: 1
DRWN 8 Drawing Figure(s); 5 Drawing Page(s)
LN.CNT 3405
CAS INDEXING IS AVAILABLE FOR THIS PATENT.

AB Methods of introducing genetic material into cells of an individual and compositions and kits for practicing the same are disclosed. The methods comprise the steps of contacting cells of an individual with a genetic vaccine facilitator and administering to the cells, a nucleic acid molecule that is free of retroviral particles. The nucleic acid molecule comprises a nucleotide sequence that encodes a protein that comprises at least one epitope that is identical or substantially similar to an epitope of a pathogen antigen or an antigen associated with a hyperproliferative or autoimmune disease, a protein otherwise missing from the individual due to a missing, non-functional or partially functioning gene, or a protein that produce a therapeutic effect on an individual. Methods of prophylactically and therapeutically immunizing an individual against HIV are disclosed. Pharmaceutical compositions and kits for practicing methods of the present invention are disclosed.

L21 ANSWER 20 OF 22 USPATFULL
AN 97:109504 USPATFULL
TI Temperature sensitive clustered changed-to-alanine **mutants** of influenza virus PB2 gene
IN Parkin, Neil T., Belmont, CA, United States
Coelingh, Kathleen L., San Francisco, CA, United States
PA Aviron, Mountain View, CA, United States (U.S. corporation)
PI US 5690937 19971125
AI US 1995-462388 19950605 (8)
DT Utility
FS Granted
EXNAM Primary Examiner: Elliott, George C.; Assistant Examiner: McKelvey, Terry A.
LREP Cserr, Luann, Dunn, Tracy
CLMN Number of Claims: 4
ECL Exemplary Claim: 1
DRWN No Drawings
LN.CNT 1306
CAS INDEXING IS AVAILABLE FOR THIS PATENT.
AB Recombinant PB2 variant influenza viruses, RNA, cDNA and vectors are provided. Also provided are immunogenic compositions containing the variant viruses, methods of producing such viruses and methods for the prophylactic treatment of influenza in humans.

L21 ANSWER 21 OF 22 USPATFULL
AN 96:108843 USPATFULL
TI Recombinant negative strand RNA virus
IN Palese, Peter, Leonia, NJ, United States
Parvin, Jeffrey D., Belmont, MA, United States
Krystal, Mark, Leonia, NJ, United States
PA Aviron, Inc., Mountain View, CA, United States (U.S. corporation)
PI US 5578473 19961126
AI US 1994-209178 19940310 (8)
DCD 20091124
RLI Division of Ser. No. US 1994-190698, filed on 1 Feb 1994, now abandoned which is a continuation of Ser. No. US 1992-925061, filed on 4 Aug 1992, now abandoned which is a division of Ser. No. US 1990-527237, filed on 22 May 1990, now patented, Pat. No. US 5166057, issued on 24 Nov 1992 which is a continuation-in-part of Ser. No. US 1989-440053, filed on 21 Nov 1989, now abandoned which is a continuation-in-part of Ser. No. US 1989-399728, filed on 28 Aug 1989, now abandoned
DT Utility
FS Granted
EXNAM Primary Examiner: Mosher, Mary E.
LREP Pennie & Edmonds
CLMN Number of Claims: 11
ECL Exemplary Claim: 1
DRWN 31 Drawing Figure(s); 20 Drawing Page(s)
LN.CNT 2842
CAS INDEXING IS AVAILABLE FOR THIS PATENT.
AB Recombinant negative strand virus RNA templates which may be used to express heterologous gene products and/or to construct chimeric viruses are described. Influenza viral polymerase, which was prepared depleted of viral RNA, was used to copy small RNA templates prepared from plasmid-encoded sequences. Template constructions containing only the 3' end of genomic RNA were shown to be efficiently copied, indicative that the promoter lay solely within the 15 nucleotide 3' terminus. Sequences not specific for the influenza vital termini were not copied, and, surprisingly, RNAs containing termini identical to those from plus sense cRNA were copied at low levels. The specificity for recognition of the virus-sense promoter was further defined by site-specific mutagenesis. It was also found that increased levels of vital protein were required in order to catalyze both the cap-endonuclease primed and primer-free

RNA synthesis from these model templates as well as from genomic length RNAs. This indicated that this reconstituted system had catalytic properties very smilar to those of native viral RNPs. High levels of expression of a heterologous gene was obtained using the constructs and methods described.

L21 ANSWER 22 OF 22 USPATFULL
AN 92:92667 USPATFULL
TI Recombinant negative strand RNA virus expression-systems
IN Palese, Peter, Leonia, NJ, United States
Parvin, Jeffrey D., Belmont, MA, United States
Krystal, Mark, Leonia, NJ, United States
PA The Mount Sinai School of Medicine of The City University of New York, New York, NY, United States (U.S. corporation)
PI US 5166057 19921124
AI US 1990-527237 19900522 (7)
RLI Continuation-in-part of Ser. No. US 1989-440053, filed on 21 Nov 1989, now abandoned And Ser. No. US 1989-399728, filed on 28 Aug 1989, now abandoned
DT Utility
FS Granted
EXNAM Primary Examiner: Schwartz, Richard A.; Assistant Examiner: Mosher, Mary E.
LREP Pennie & Edmonds
CLMN Number of Claims: 35
ECL Exemplary Claim: 1
DRWN 31 Drawing Figure(s); 20 Drawing Page(s)
LN.CNT 2742
CAS INDEXING IS AVAILABLE FOR THIS PATENT.
AB Recombinant negative strand virus RNA templates which may be used to express heterologous gene products and/or to construct chimeric viruses are described. Influenza viral polymerase, which was prepared depleted of viral RNA, was used to copy small RNA templates prepared from plasmid-encoded sequences. Template constructions containing only the 3' end of genomic RNA were shown to be efficiently copied, indicative that the promoter lay solely within the 15 nucleotide 3' terminus. Sequences not specific for the influenza viral termini were not copied, and, surprisingly, RNAs containing termini identical to those from plus sense cRNA were copied at low levels. The specificity for recognition of the virus-sense promoter was further defined by site-specific mutagenesis. It was also found that increased levels of viral protein were required in order to catalyze both the cap-endonuclease primed and primer-free RNA synthesis from these model templates as well as from genomic lengths RNAs. This indicated that this reconstituted system had catalytic properties very similar to those of native viral RNPs. High levels of expression of a heterologous gene was obtained using the constructs and methods described.

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